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FIGURE 1

1	ATGTCAGTGGAGCCATGAAGAAGGGAGTGGGAGGGCAGTTGGGCTTGGAGGCGGCAGC	60
61	GGCTGCCAGGCTACGGAGGAAGACCCCTTCCGACTGCGGGGCTTGCCTCCGGGACAA	120
121	GGTGGCAGGCGCTGAGGGCTGCCGACGCCCTGCGTGGTGGAGGGGAGCTCAGCTCGGTTG	180
181	TGGGAGCAGGCGACCGGCACCTGGCTGGATGGACCTGGAAGCCTCGCTGCTGCCACATGGT	240
241	CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCAGCAGGATCACCTCCT	300
301	CGCACGGGAGGATCTCTACATCAACATCATCATGCCTTCGGTGTTCGGCACCATCTGC	360
361	CTCCTGGGCATCATCCGGAACTCCACGGTCATCTTCGCGGTCGTGAAGAAGTCCAAAGCTG	420
421	CAC TGGTGCAACAACCTCCCGACATCTTTCATCATCAACCTCTCGGTAGTAGATCTCCTC	480
481	TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT	540
541	GGGAGAGCCATGTGCAACCTCATCACGGCCATGGATGCCAATAGTCAGTTCAACCAGCACC	600
601	TACATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC	660
661	ACGAAGTTCCGGAAGCCCTCTGTGGCCACCCCTGGTGATCTGCCCTCCTGTGGGCCCTCTCC	720
721	TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCCAGGAGGTGCA	780
781	GTGGGCTGGGGCATACGCCCTGCCCAACCCAGACACTGACCTCTACTGGTTCAACCCTGTAC	840
841	CAGTTTTCCTGGCCCTTGCCCTGCCCTTTGTGGTCATCACAGCCGCATACGTGAGGATC	900
901	CTGCAGGCGCATGACCTCCCTCAGTGGCCCCCGCCCTCCAGCGCAGCATCCGGCTGCCGACA	960
961	AAGAGGTGACCCGCACAGCCATCGCCATCTGTCTGGTCTTCTTTGTGTGCTGGGCACCC	1020
1021	TACTATGTGCTACAGTGAACCCAGTTGTCCATCAGCCGCCCGACCCCTCACCTTTGTCTAC	1080
1081	TTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTTGTGTAC	1140
1141	ATCGTGCTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGGTGAAGCCTGCAGCCCCAG	1200
1201	GGCAGCTTCGGCTTTCAGCAACGCTCAGACGGCTGACGAGGAGGAGACAGAAAGCAAA	1260
1261	GGCACCTGA	1269

FIGURE 2

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FIGURE 3

1 MSVGAMKKGVGRAVGLGGGS 20
21 GCQATEEDPLPDCGACAPGQ 40
41 GGRRWRLPQPAWVEGSSARL 60
61 WEQATGTGWMDLEASLLPTG 80
81 PNASNTSDGPDNLTSA GSPF 100
101 RTGSISYIN IIMPSEGTIC 120
121 ILGIGNSTVIEAVVKKSKL 140
141 HWCNNVPD IEIINISVVDLI 160
161 ELLGMEFMIHQLMGNGVWHF 180
181 GETMCTLITAMD ANSOETST 200
201 YIITAMAI ^{III} DRYLATVHPIS S 220
221 TKFRKPS VATLVICLLWALS 240
241 FISITPVWLYARLI ^{IV} PFPGGA 260
261 VGC G I R L P N F D T D L Y W F T L Y 280
281 Q F F L A F A L P F V V I T A A V V P I 300
301 LQRMES SVAPASQRSIRLRT 320
321 KR V T E T A I A I C L V F F V C W A P 340
341 Y Y V L O L T O L S I S R P T L T F V Y 360
361 LYNAAISLG Y A N S C L N P F V Y 380
381 I V L C E T F R K R L V L S V K P A A Q 400
401 GQLRAVSNAQTAD EERTESK 420
421 GT 422

FIGURE 4

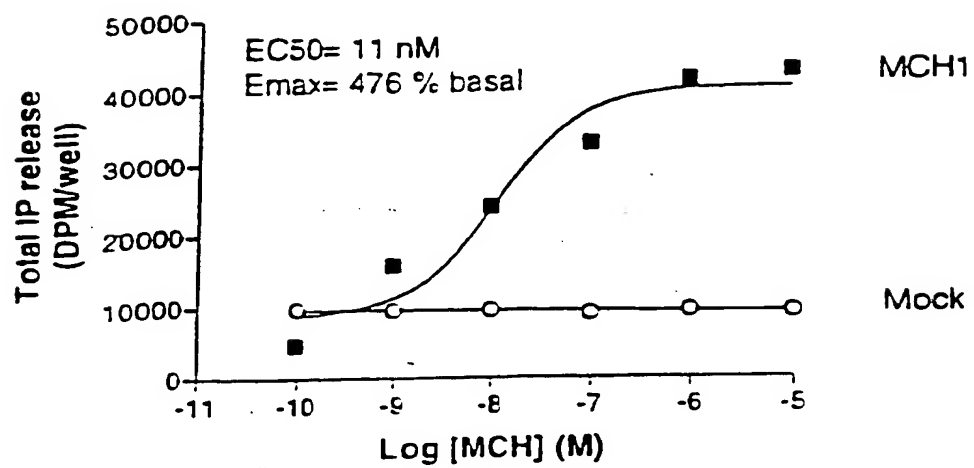
1	GCAGGGACCTGCACCGGCTGCATGGATCTGCAACCTCGTTGCTGTCCACTGGCCCCAA	60
61	TGCCAGCAACATCTCCGATGGCCAGGATAATCTCACATTGCCGGGGTACCTCCTCGCAC	120
121	AGGGAGTGTCTCTACATCAACATCATATATGCCCTTCGGTGTGGTACCATCTGTCTCCT	180
181	GGGCATCGTGGGAACCTCCACGGTCATCTTTGCTGTGGTGAAGAAGTCCAAAGCTACACTG	240
241	GTGCAGCAACGTCCCCGACATCTTCATCATCAACCTCTCTGTGGTGGATCTGCTCTTCCT	300
301	GCTGGGCATGCCCTTTCATGATCCACCAGCTCATGGGGAACGGCGTCTGGCACCTTTGGGGA	360
361	AACCATGTGCACCTCTCATACAGCCATGGACGCCAACAGTCA GTTCACTAGCACCTACAT	420
421	CCTGACTGCCCATGACCATTGACCGCTACTTTGGCCACCGTCCACCCCATCTCCTCCACCNA	480
481	GTTCGGGAAGCCCTCCATGGCCACCCCTGGTGATCTGCCCTCCTGTGGGCGCTCTCCTTCAT	540
541	CAGTATCACCCCTGTGGCTCTACGCCAGGCTCATTCCTTCCCAGGGGGTGTGTGGG	600
601	CTGTGGCATCCGCCCTGCCAAACCCGGACACTGACCTCTACTGGTTCACTCTGTACCA GTT	660
661	TTTCCTGGCCTTTGCCCTTCCGTTTGTGGTCATTACCGCCGCATACGTGAAATACTACA	720
721	GCGCATGACGTCTTCGGTGGCCCCAGCCTCCCAACGCAGCATCCGGCTTCGGACAAAGAG	780
781	GGTGACCCGCACGGCCATTGGCCATCTGTCTGGTCTTCTTTGTGTGCTGGCACCCCTACTA	840
841	TGTGCTGCAGCTGACCCAGCTGTCCATCAGCCGCCGACCCCTCACGTTTGTCTACTTGT	900
901	CAACGGGGCCATCAGCTTGGGCTATGCTAACAGCTGCCCTGAACCCCTTTGTGTACATAGT	960
961	GCTCTGTGAGACCTTTCCGAAACGGCTTGGTGTGTCAGTGAAAGCCTGCAGCCCCAGGGCA	1020
1021	GCTCCGCACGGTCAGCAACGCTCAGACAGCTGATGAGGAGAGGACAGAAAGCAAGGCAC	1080
1081	CTGACAAATCCCCAGTCCCTCCAAAGTCAGGCCACCCCATCAAAACCGTGGGGAGAGATAC	1140
1141	TGAGATTAAACCCAAAGGCTACCTGGGAGAAATGCAGAGGCTGGGAGGCTGGGGGCTTGTAG	1200
1201	CAACCACATTCCAC	1214

FIGURE 5

1	M	D	L	Q	T	S	L	L	S	T	G	P	N	A	S	N	I	S	D	G	20
21	Q	D	L	L	T	S	L	L	S	T	G	P	N	A	S	N	I	S	D	G	40
41	I	M	P	P	S	V	F	G	T	I	C	L	H	L	G	V	G	N	S	T	60
61	V	I	A	A	V	V	K	K	S	D	L	L	F	L	C	N	V	P	D	I	80
81	F	I	I	I	L	S	V	V	D	L	L	F	L	L	G	M	F	F	M	I	100
101	H	Q	L	M	G	N	S	Q	F	T	S	T	Y	I	L	T	A	M	T	I	120
121	A	M	D	A	N	S	V	H	F	I	S	S	T	K	F	R	K	P	S	M	140
141	R	Y	L	A	T	V	L	P	A	G	L	S	F	I	S	I	T	P	V	W	160
161	T	L	V	I	C	L	P	F	G	L	A	V	G	F	I	G	I	R	L	P	180
181	T	A	R	L	I	P	F	P	G	L	A	V	G	F	I	G	I	R	L	P	200
201	P	D	T	D	L	Y	W	F	T	V	K	I	Q	R	M	T	S	S	V	A	220
221	F	V	V	I	T	A	A	F	V	L	R	P	Y	L	R	T	R	T	A	I	240
241	P	A	S	Q	R	S	I	V	C	W	A	P	Y	L	Y	V	L	Q	L	T	260
261	I	C	L	V	F	F	V	C	T	F	A	V	Y	L	Y	N	A	C	R	G	280
281	S	I	S	R	P	T	L	N	F	F	A	V	Y	L	Y	N	A	C	R	K	300
301	Y	A	N	S	C	S	E	R	P	F	A	V	Y	L	Y	N	A	C	R	K	320
321	R	L	V	L	E	E	R	P	F	A	V	Y	L	Y	N	A	C	R	K	K	340
341	Q	T	A	D	E	E	R	P	F	A	V	Y	L	Y	N	A	C	R	K	K	354

FIGURE 6

IP release in MCH1- and
mock-transfected Cos-7 cells



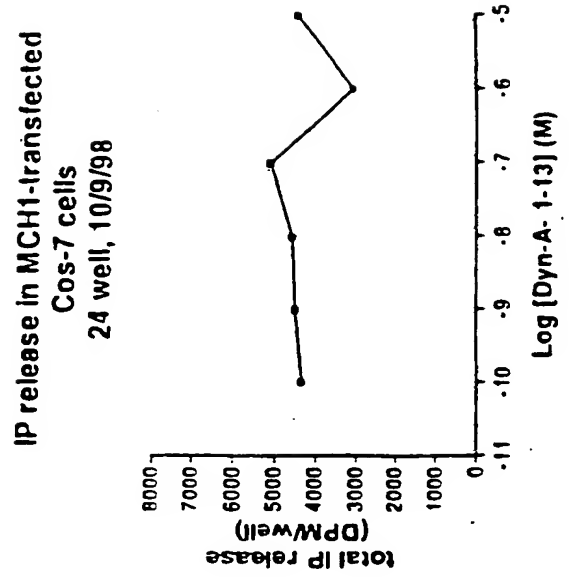
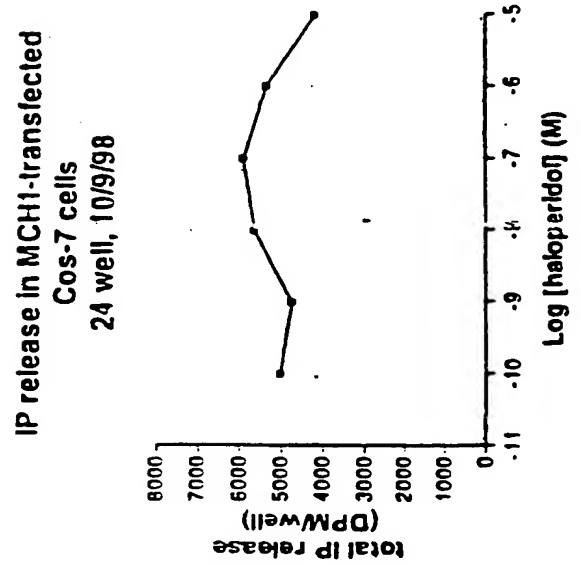
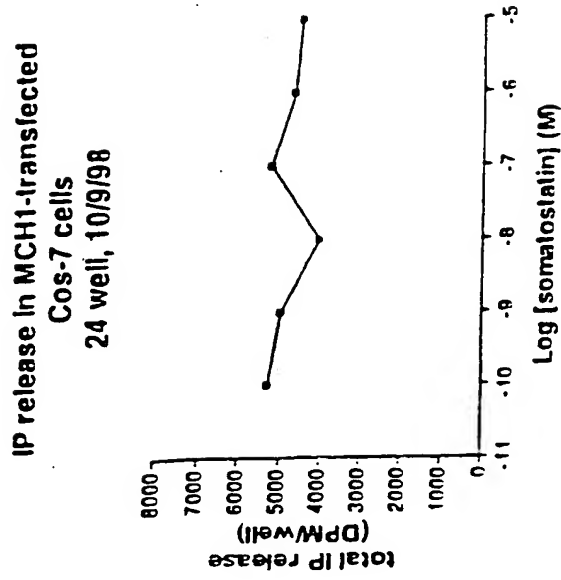
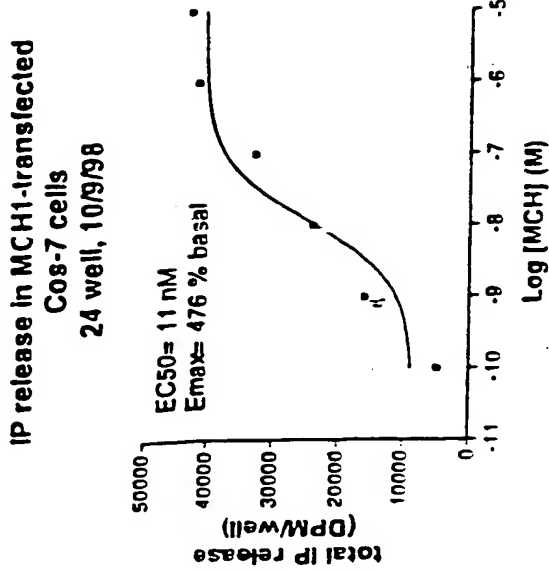


FIGURE 7

Microphysiometer Response
CHO cells

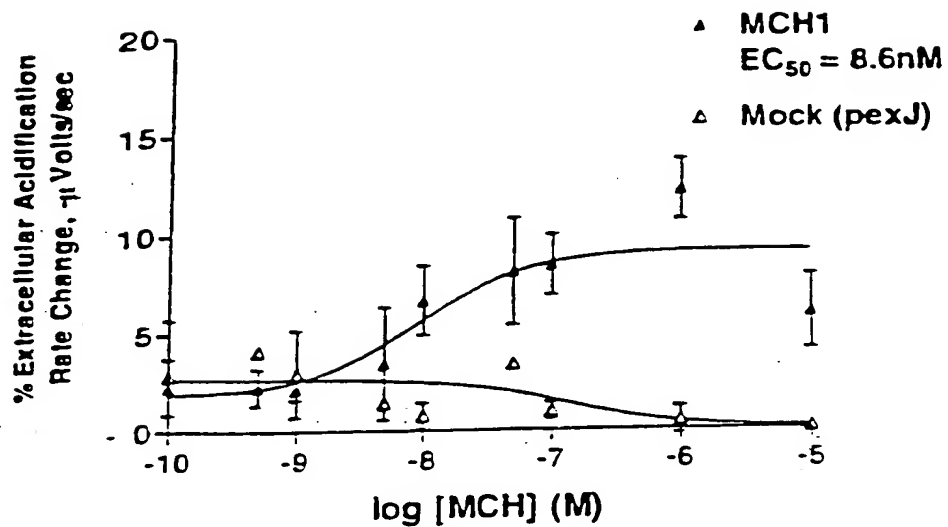
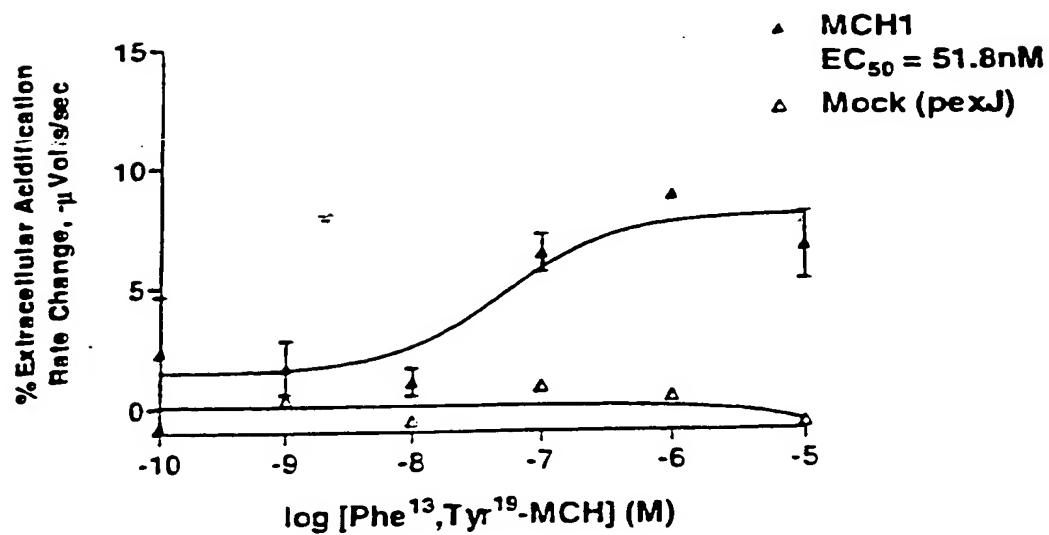


FIGURE 8

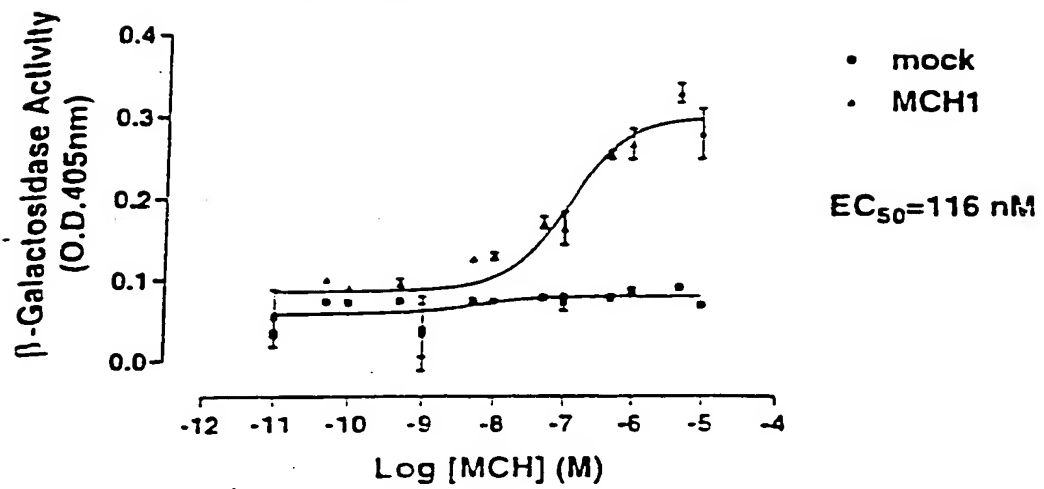
Microphysiometer Response
CHO cells



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FIGURE 9

Agonist-Mediated c-fos- β -gal
Activity in Cos-7 Cells



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FIGURE 10

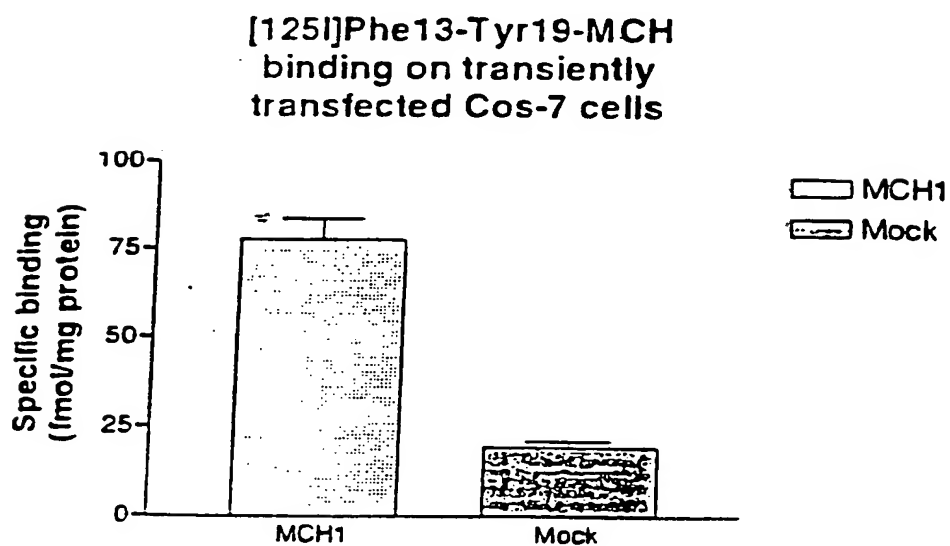
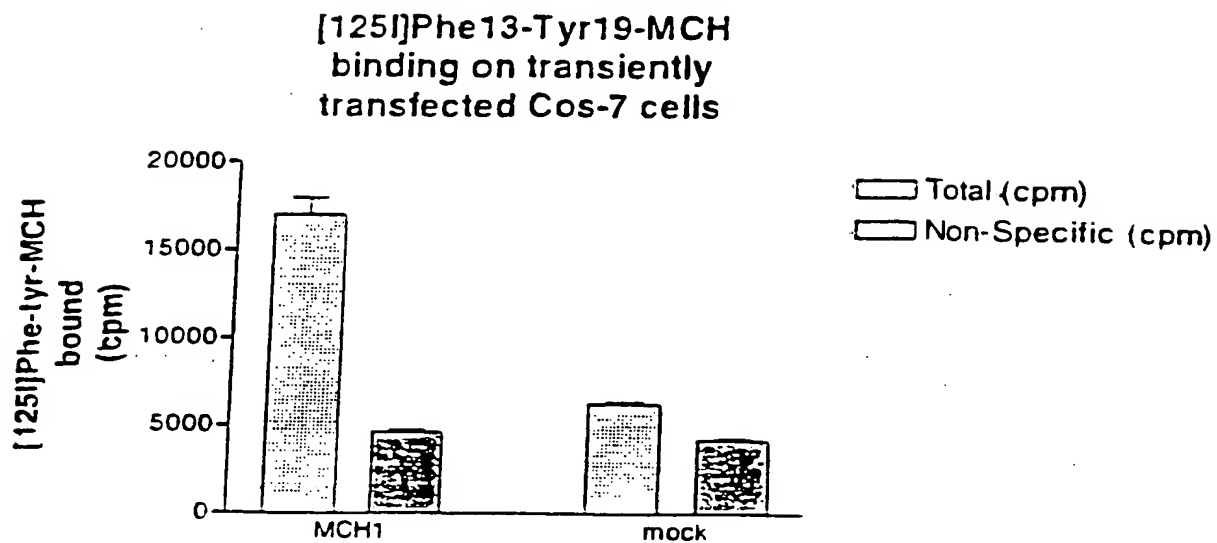


FIGURE 11

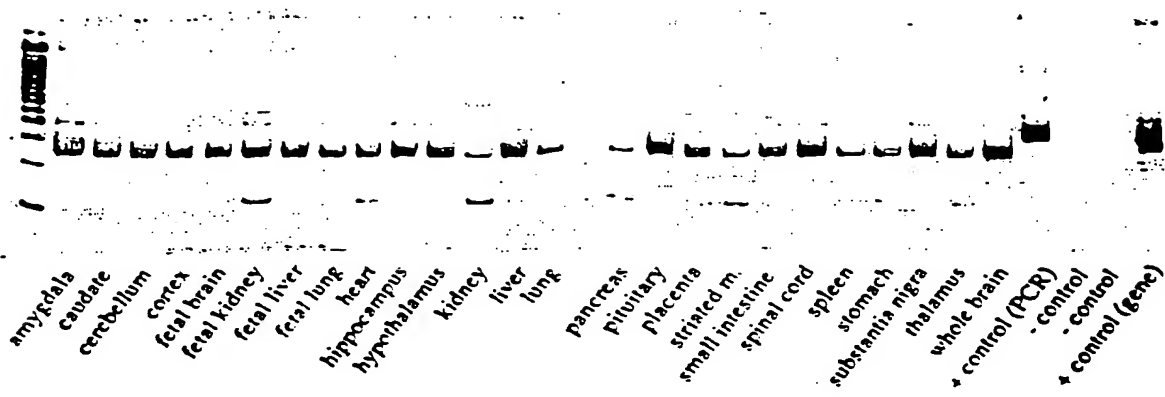


Figure 12

	1			40
TL231	MSVGAMKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ
R106	MSVGAMKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ
R114	MSVGAaKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ
BO120	~~~~~	~~~~~	~~~~~	~~~~~
	41			80
TL231	GGRRWRLPQP	AWVEGSSARL	WEQATGTGWM	DLEASLLPTG
R106	GGRRWRLPQP	AWVEGSSARL	WEQATGTGWa	DLEASLLPTG
R114	GGRRWRLPQP	AWVEGSSARL	WEQATGTGWa	DLEASLLPTG
BO120	~~~~~	~~~~~	~~~~~M	DLEASLLPTG
	81		100	
TL231	PNASNTSDGP	DNLTSAGSPP...		
R106	PNASNTSDGP	DNLTSAGSPP...		
R114	PNASNTSDGP	DNLTSAGSPP...		
BO120	PNASNTSDGP	DNLTSAGSPP...		

[illegible]

[illegible]

1	M	D	L	E	A	S	L	L	P	T	G	P	N	A	S	I	T	S	D	G	20
21	P	D	N	L	T	S	A	G	S	P	P	R	T	G	S	I	I	G	N	I	40
41	I	M	P	S	V	F	G	T	I	C	L	H	L	G	I	N	V	P	D	I	60
61	V	I	F	V	V	K	K	S	K	L	L	F	L	C	N	N	M	P	F	M	80
81	F	I	I	N	L	S	V	D	L	L	F	G	E	L	M	C	T	L	I	T	100
101	H	Q	L	M	G	N	G	V	W	H	F	G	E	L	T	R	A	M	I	D	120
121	A	M	D	A	N	S	Q	F	T	S	T	Y	I	F	R	K	P	S	V	A	140
141	R	Y	L	A	T	V	H	F	I	S	S	T	K	F	I	S	I	T	P	V	160
161	T	L	V	I	C	L	L	W	A	L	S	F	I	S	C	I	G	L	R	P	180
181	Y	A	R	L	I	P	F	P	G	G	A	V	G	F	I	G	L	I	F	A	200
201	P	D	T	D	I	L	Y	W	F	T	L	Y	Q	F	F	L	M	T	S	V	220
221	F	V	V	I	T	A	A	F	Y	R	I	L	Q	R	V	M	T	R	S	A	240
241	P	A	S	Q	R	F	I	V	R	L	R	A	P	Y	V	N	L	Q	A	T	260
261	I	C	L	V	F	F	V	C	W	F	A	P	Y	L	Y	V	N	L	A	C	280
281	S	I	S	R	P	T	L	N	P	F	V	Y	Y	I	G	Q	T	A	E	V	300
301	Y	A	N	S	C	S	V	E	R	T	S	K	G	G	T	L	S	F	N	A	320
321	R	L	V	L	E	E	R	T	E	S	K	G	G	T	L	S	F	N	A	A	340
341	Q	T	A	D	E	E	R	T	E	S	K	G	G	T	L	S	F	N	A	A	353